

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application.

These amendments introduce no new matter and support for the amendment is replete throughout the specification and claims as originally filed. These amendments are made without prejudice and are not to be construed as abandonment of the previously claimed subject matter, or agreement with any objection or rejection of record.

Listing of Claims:

Claims 1 to 30 (Cancelled).

31. (previously presented) A composition comprising a protein, wherein the protein comprises two or more redox active amino acids selected from the group consisting of: a 3,4-dihydroxy-L-phenylalanine (DHP), a 3,4,5-trihydroxy-L-phenylalanine, a 3-nitro-tyrosine, a 4-nitro-phenylalanine, and a 3-thiol-tyrosine.

32. (cancelled)

33. (currently amended) The composition of claim 31, wherein the protein comprises an amino acid sequence that is at least 95%~~75%~~ identical to that of a wild-type therapeutic protein, a diagnostic protein, an industrial enzyme, or portion thereof.

34. (original) The composition of claim 31, wherein the composition comprises a pharmaceutically acceptable carrier.

35. (previously presented) The composition of claim 31, wherein the protein further comprises at least one unnatural amino acid that is not a 3,4-dihydroxy-L-phenylalanine (DHP), a 3,4,5-trihydroxy-L-phenylalanine, a 3-nitro-tyrosine, a 4-nitro-phenylalanine, or a 3-thiol-tyrosine.

36. (cancelled)

37. **(previously presented)** The composition of claim 31, wherein the two or more redox active amino acids are the same.

38. **(previously presented)** The composition of claim 31, wherein at least two of said redox active amino acids are different.

39. **(previously presented)** The composition of claim 31, wherein the protein comprises a myoglobin polypeptide or a portion thereof.

40. **(cancelled)**

41. **(previously presented)** The composition of claim 31, wherein the protein is capable of undergoing oxidation.

42. **(previously presented)** The composition of claim 31, wherein the protein is capable of undergoing (i) oxidation or (ii) a shift in reductive peak potential as measured by voltammetric response in comparison to a corresponding protein that lacks said at least two redox active amino acids, and wherein said oxidation or shift in reductive peak potential require said at least two redox active amino acids.

43. **(previously presented)** The composition of claim 31, wherein at least one of said two or more redox active amino acids is 3,4-dihydroxy-L-phenylalanine (DHP).

44. **(previously presented)** The composition of claim 31, wherein the redox active amino acid is a redox catalyst.

45. **(Currently amended)** The composition of claim 31, further comprising:

i) at least one orthogonal tRNA (O-tRNA), wherein the O-tRNA comprises or is encoded by a polynucleotide sequence as set forth in SEQ ID NO.: 2, or a complementary polynucleotide sequence thereof;

ii) at least one orthogonal aminoacyl- tRNA synthetase (O-RS) comprising or derived from an RS selected from the group consisting of: an *Archaeoglobus fulgidus* synthetase, a *Methanosarcina mazei* synthetase, a *Methanobacterium thermoautotrophicum* synthetase, and a *Pyrococcus horikoshii* synthetase, wherein the O-RS preferentially aminoacylates the O-tRNA with the redox active amino acid; and

- iii) a nucleic acid that encodes the protein, wherein the nucleic acid comprises at least two selector codons that are recognized by the O-tRNA.

46. (Currently amended) The composition of claim 31, further comprising an O-RS comprising an amino acid sequence comprising SEQ ID NO.: 1, ~~or a conservative variant thereof.~~

47. (Currently amended) The composition of claim 31, further comprising an ~~O-RS that has an efficiency in a translation system that is at least 50% of the efficiency observed in a translation system comprising an O-tRNA,~~ an aminoacyl-tRNA synthetase comprising the amino acid sequence of SEQ ID NO: 1 that preferentially aminoacylates the O-tRNA with at least one of the two or more redox active amino acids, and a nucleic acid encoding a polypeptide of interest, said nucleic acid comprising at least one selector codon that is recognized by the O-tRNA.